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RAW SEQUENCE LISTING PATENT APPLICATION US/09/804,625

DATE: 01/11/200 TIME: 22:10:28

INPUT SET: S36715.raw

#3

This Raw Listing contains the General Information Section and up to the first 5 pages.

1	SEQUENCE LISTING
2 3	(1) General Information:
4	
5	(i) APPLICANT: Wang, Elizabeth A.
6	Rosen, Vicki A. Wozney, John M ROSEN A. Wozney, John M
7 8	Wozney, John M
9	(ii) TITLE OF INVENTION: Novel BMP Products
10	(11) IIIII of Liverillon, novel bill flowdood
11	(iii) NUMBER OF SEQUENCES: 6
12	
13	(iv) CORRESPONDENCE ADDRESS:
14	(A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
15	(B) STREET: 87 CAMBRIDGEPARK DRIVE
16	(C) CITY: CAMBRIDGE
17	(D) STATE: MA
18	(E) COUNTRY: USA
19	(F) ZIP: 02140
20	(-) COMPUTED DELDIDIT DODA
21	(v) COMPUTER READABLE FORM:
22 23	(A) MEDIUM TYPE: Floppy disk
23 24	(B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25	(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26	(b) borname. rateletin kerease #1.0, version #1.25
27	(vi) CURRENT APPLICATION DATA:
28	(A) APPLICATION NUMBER: 09/804,625
29	(B) FILING DATE:
30	(C) CLASSIFICATION:
31	
32	(vii) PRIOR APPLICATION DATA:
33	(A) APPLICATION NUMBER: 08/925,779
34	(B) FILING DATE:
35	
36	
37	(viii) ATTORNEY/AGENT INFORMATION:
38	(A) NAME: Kapinos, Ellen J.
39 40	(B) REGISTRATION NUMBER: 32,245 (C) REFERENCE/DOCKET NUMBER: 5160C
41	(C) REFERENCE/DOCKET NUMBER: 5160C
42	(ix) TELECOMMUNICATION INFORMATION:
43	(A) TELEPHONE: 617-876-1170
44	(B) TELEFAX: 617-876-5851
45	(,

RAW SEQUENCE LISTING PATENT APPLICATION US/09/804,625

DATE: 01/11/2002 TIME: 22:10:28

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	•	•				INFUL SELL	330/13.1uw
47	(2) INFO	RMATION FOR S	EQ ID NO:1:				
48 49 50 51 52 53	(i)	(B) TYPE: n	592 base p ucleic acid DNESS: doub	airs			
54 55 56	(ii)	MOLECULE TYP	E: DNA (gen	omic)			
57 58	(iii)	HYPOTHETICAL	: NO				
59	(iv)	ANTI-SENSE:	NO				
60 61 62	(vi)	ORIGINAL SOU (A) ORGANIS	RCE: M: BOS TAUR	us			
63 64 65 66 67	(vii)		OURCE: : BOVINE GE LAMBDA BP-2		AMBDA J1		
68 69 70	(viii)	POSITION IN (C) UNITS:					
71 72 73 74	(ix)	FEATURE: (A) NAME/KE (B) LOCATIO					
75 76 77 78	(ix)	FEATURE: (A) NAME/KE (B) LOCATIO	Y: mat_pept N: 46387	ide	·		
80 81	(xi)	SEQUENCE DES	CRIPTION: S	EQ ID NO:1	:		
82 83 84 85		GAT GGG AAA G Asp Gly Lys G		Leu His Ar			48
86 87 88 89		CAC AAA CAG C His Lys Gln A 5					96
90 91 92 93		TAT GTG GAC T Tyr Val Asp F 20					144
94 95 96 97		CCG GGG TAT C Pro Gly Tyr H					192
98 99		GCC GAT CAC C Ala Asp His L					240

RAW SEQUENCE LISTING PATENT APPLICATION US/09/804,625

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100	50	•		•		55	•				60		•			65	
101	-																
102				TCA													288
103	Leu	Val	Asn	Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	
104					70					75					8,0		
105																	
106	ACA	GAG	CTC	AGC	GCC	ATC	TCC	ATG	CTG	TAC	CTT	GAT	GAG	AAT	GAG	AAG	336
107	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	Glu	Asn	Glu	Lys	
108				85					90	_				95			
109																	
110	GTG	GTA	TTA	AAG	AAC	TAT	CAG	GAC	ATG	GTT	GTC	GAG	GGT	TGT	GGG	TGT	384
111				Lys													
112			100	-		-		105					110	_	_		
113																	
114	CGT	TAG	CACA	GCA Z	TAAA	AAAA	ra T	AAAT	ATATA	A TA	CATA?	CATA	TTA	SAAA	AAC		437
115	Arg																
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117																	
118	AGC	ממממ	מ מ מ	דר אם מ	ቲጥጥ ር /	AC AC	יייייייייייייייייייייייייייייייייייייי	'אדא	г тт	CCCA	ATGA	AGA	CTTT	ATT '	TATG	GAATGG	497
119	AGC			10111	31102												
120	አ ልጥ(ZCAC	מ מ מ	ממממ	<u> </u>	מים מיי	ДССТ	יידידידי	r GA	ΔΔΔΟ	בדבי	ттти	TAT	CTA (CCGA	AAAGAA	557
121	TALL!	JOAG		LIGIL		· · ·	10011		. 0								
121	Cirrino	יייי אי	7 7 7 A	CAAA'	ייייי איז	מידייו	מיירא	2262	מידים ב	יייית							592
123	GII	JUUA	man.	CAAA.	ini.	II M	11 CM	37.07.0									
123			••														
125	(2)	TNE	ODMA	TION	₽ ∩₽	GEO.	TD I	MO • 2									
	(4)	TME	OKUM	TION	FOR	SEQ	110	10.2	•								
126			/i)	e eati	ence	CHVI	ラ	יסדפי	יידרפ								
127			(i)	SEQUI							2						
127 128			(i)	(A) LEI	NGTH	: 12:	9 am:	ino a		S						
127 128 129			(i) :	(A (B) LEI) TYI	NGTH PE: a	: 12: amin	9 am.	ino a id		5						
127 128 129 130			(i) :	(A (B) LEI	NGTH PE: a	: 12: amin	9 am.	ino a id		5						
127 128 129 130 131			, ,	(A (B (D) LEI) TYI) TOI	NGTH PE: 6 POLO	: 12: amino GY: :	9 am o ac line	ino a id ar		5						
127 128 129 130 131			, ,	(A (B) LEI) TYI) TOI	NGTH PE: 6 POLO	: 12: amino GY: :	9 am o ac line	ino a id ar		5						
127 128 129 130 131 132 133		(ii)	(A (B (D MOLE) LEI) TYI) TOI	NGTH PE: 6 POLOG	: 12: amino GY: :	9 am o ac line rote	ino a id ar in	acid							
127 128 129 130 131 132 133		(ii)	(A (B (D) LEI) TYI) TOI	NGTH PE: 6 POLOG	: 12: amino GY: :	9 am o ac line rote	ino a id ar in	acid		2:					
127 128 129 130 131 132 133 134 135	Cl	(; ;	ii) xi)	(A (B (D MOLE SEQU) LEI) TYI) TOI CULE	NGTH PE: 6 POLOG TYPI DESG	: 12: amino GY: : E: p: CRIP	9 am. o ac. line rote	ino a id ar in : SE	acid:	NO:		Glu.	Ive	Ara	Gln	
127 128 129 130 131 132 133 134 135	_	(; ;	ii) xi)	(A (B (D MOLE SEQU) LEI) TYI) TOI CULE	NGTH PE: 6 POLOG TYP) DESG Gly	: 12: amino GY: : E: p: CRIP	9 am. o ac. line rote	ino a id ar in : SE	acid:	NO:		Glu	Lys	Arg	Gln 1	
127 128 129 130 131 132 133 134 135 136	Gly	(: :	ii) xi)	(A (B (D MOLE SEQU) LEI) TYI) TOI CULE	NGTH PE: 6 POLOG TYPI DESG	: 12: amino GY: : E: p: CRIP	9 am. o ac. line rote	ino a id ar in : SE	acid:	NO:		Glu	Lys	Arg	Gln 1	
127 128 129 130 131 132 133 134 135 136 137	-15	((: His	ii) xi) Asp	(A (B (D MOLE SEQUI) LEI) TYI) TOI CULE ENCE Lys	NGTH PE: 6 POLOG TYP DESG Gly -10	: 12: amino GY: : E: p: CRIP	9 am. o ac line rote TION Pro	ino a id ar in : SEG	acid Q ID His	NO:2	Arg				1	
127 128 129 130 131 132 133 134 135 136 137 138	-15	((: His	ii) xi) Asp	(A (B (D MOLE SEQUI Gly) LEI) TYI) TOI CULE ENCE Lys	NGTH PE: 6 POLOG TYP DESG Gly -10	: 12: amino GY: : E: p: CRIP	9 am. o ac line rote TION Pro	ino a id ar in : SE0 Leu	acid Q ID His	NO:2	Arg		Lys		1	
127 128 129 130 131 132 133 134 135 136 137 138 139 140	-15	((: His	ii) xi) Asp	(A (B (D MOLE SEQUI) LEI) TYI) TOI CULE ENCE Lys	NGTH PE: 6 POLOG TYP DESG Gly -10	: 12: amino GY: : E: p: CRIP	9 am. o ac line rote TION Pro	ino a id ar in : SEG	acid Q ID His	NO:2	Arg				1	
127 128 129 130 131 132 133 134 135 136 137 138 139 140	-15 Ala	(His Lys	ii) xi) Asp His	(A (B (D MOLE SEQUI Gly Lys 5) LEI) TYI) TOI CULE ENCE Lys	NGTH PE: 6 POLOG TYPI DESG Gly -10 Arg	: 12: amino GY: : E: p: CRIP' His	9 am. c ac. line rote rote Pro Arg	ino a id ar in : SEG Leu Leu	acid Q ID His Lys	NO:2 Arg -5 Ser	Arg Ser	Cys	Lys 15	Arg	1 His	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141	-15 Ala	(His Lys	ii) xi) Asp His	(A (B (D MOLE SEQUI Gly) LEI) TYI) TOI CULE ENCE Lys	NGTH PE: 6 POLOG TYPI DESG Gly -10 Arg	: 12: amino GY: : E: p: CRIP' His	9 am. c) ac. line. rote. FION Pro Arg	ino a id ar in : SEG Leu Leu	acid Q ID His Lys	NO:2 Arg -5 Ser	Arg Ser	Cys	Lys 15	Arg	1 His	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143	-15 Ala	(His Lys	ii) xi) Asp His	(A (B (D MOLE SEQUI Gly Lys 5) LEI) TYI) TOI CULE ENCE Lys	NGTH PE: 6 POLOG TYPI DESG Gly -10 Arg	: 12: amino GY: : E: p: CRIP' His	9 am. c ac. line rote rote Pro Arg	ino a id ar in : SEG Leu Leu	acid Q ID His Lys	NO:2 Arg -5 Ser	Arg Ser	Cys	Lys 15	Arg	1 His	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	-15 Ala Pro	((: His Lys Leu	ii) xi) Asp His Tyr 20	(A (B (D MOLE SEQUI Gly Lys 5 Val) LEI) TY!) TO! CULE ENCE Lys Gln	MGTH PE: A POLOG TYP DESG Gly -10 Arg Phe	: 12: amind GY: : E: p: CRIP His Lys Ser	9 am b ac cline rote TION Pro Arg Asp 25	ino aid ar in EEu Leu 10 Val	Q ID His Lys Gly	NO:2 Arg -5 Ser Trp	Arg Ser Asn	Cys Asp 30	Lys 15 Trp	Arg	1 His Val	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145	-15 Ala Pro	() His Lys Leu Pro	ii) xi) Asp His Tyr 20	(A (B (D MOLE SEQUI Gly Lys 5 Val) LEI) TY!) TO! CULE ENCE Lys Gln	MGTH PE: A POLOG TYP DESG Gly -10 Arg Phe	: 12: amind GY: : E: p: CRIP His Lys Ser	9 am b ac cline rote TION Pro Arg Asp 25	ino aid ar in EEu Leu 10 Val	Q ID His Lys Gly	NO:2 Arg -5 Ser Trp	Arg Ser Asn	Cys Asp 30	Lys 15 Trp	Arg	1 His	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146	-15 Ala Pro	((: His Lys Leu	ii) xi) Asp His Tyr 20	(A (B (D MOLE SEQUI Gly Lys 5 Val) LEI) TY!) TO! CULE ENCE Lys Gln	MGTH PE: A POLOG TYP DESG Gly -10 Arg Phe	: 12: amind GY: : E: p: CRIP His Lys Ser	9 am b ac cline rote TION Pro Arg Asp 25	ino aid ar in EEu Leu 10 Val	Q ID His Lys Gly	NO:2 Arg -5 Ser Trp	Arg Ser Asn	Cys Asp 30	Lys 15 Trp	Arg	1 His Val	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147	-15 Ala Pro Ala	(His Lys Leu Pro	ii) xi) Asp His Tyr 20	(A (B (D MOLE SEQUI Gly Lys 5 Val) LEI) TYI) TOI CULE ENCE Lys Gln Asp	MGTH PE: A POLOG TYPP DESG Gly -10 Arg Phe His	: 12: amind GY: : E: p: CRIP His Lys Ser Ala 40	9 am c) ac line rote FION Pro Arg Asp 25 Phe	ino a id ar in EEu Leu 10 Val	Q ID His Lys Gly Cys	NO:2 Arg -5 Ser Trp	Arg Ser Asn Gly 45	Cys Asp 30 Glu	Lys 15 Trp Cys	Arg Ile Pro	1 His Val Phe	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147	-15 Ala Pro Ala	(His Lys Leu Pro	ii) xi) Asp His Tyr 20	(A (B (D MOLE SEQUI Gly Lys 5 Val) LEI) TYI) TOI CULE ENCE Lys Gln Asp	MGTH PE: A POLOG TYPP DESG Gly -10 Arg Phe His	: 12: amind GY: : E: p: CRIP His Lys Ser Ala 40	9 am c) ac line rote FION Pro Arg Asp 25 Phe	ino a id ar in EEu Leu 10 Val	Q ID His Lys Gly Cys	NO:3 Arg -5 Ser Trp His	Arg Ser Asn Gly 45	Cys Asp 30 Glu	Lys 15 Trp Cys	Arg Ile Pro	1 His Val Phe	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149	-15 Ala Pro Ala	(His Lys Leu Pro	ii) xi) Asp His Tyr 20	(A (B (D MOLE SEQUI Gly Lys 5 Val) LEI) TYI) TOI CULE ENCE Lys Gln Asp	MGTH PE: A POLOG TYPP DESG Gly -10 Arg Phe His	: 12: amind GY: : E: p: CRIP His Lys Ser Ala 40	9 am c) ac line rote FION Pro Arg Asp 25 Phe	ino a id ar in EEu Leu 10 Val	Q ID His Lys Gly Cys	NO:2 Arg -5 Ser Trp	Arg Ser Asn Gly 45	Cys Asp 30 Glu	Lys 15 Trp Cys	Arg Ile Pro	1 His Val Phe	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150	-15 Ala Pro Ala Pro 50	() His Lys Leu Pro 35 Leu	ii) xi) Asp His Tyr 20 Pro	(A (B (D MOLE SEQUI Gly Lys 5 Val Gly Asp) LEI) TYI) TOI CULE ENCE Lys Gln Asp Tyr	MGTH PE: A POLOG TYPP DESG Gly -10 Arg Phe His Leu 55	: 12: amind GY: : E: p: CRIP His Lys Ser Ala 40 Asn	9 am c) ac line rote TION Pro Arg Asp 25 Phe Ser	ino aid ar in Eu Leu 10 Val	Q ID His Lys Gly Cys Asn	NO:2 Arg -5 Ser Trp His	Arg Ser Asn Gly 45	Cys Asp 30 Glu	Lys 15 Trp Cys	Arg Ile Pro Gln	His Val Phe Thr 65	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149	-15 Ala Pro Ala Pro 50	() His Lys Leu Pro 35 Leu	ii) xi) Asp His Tyr 20 Pro	(A (B (D MOLE SEQUI Gly Lys 5 Val Gly Asp) LEI) TYI) TOI CULE ENCE Lys Gln Asp Tyr	MGTH PE: A POLOG TYPP DESG Gly -10 Arg Phe His Leu 55	: 12: amind GY: : E: p: CRIP His Lys Ser Ala 40 Asn	9 am c) ac line rote TION Pro Arg Asp 25 Phe Ser	ino aid ar in Eu Leu 10 Val	Q ID His Lys Gly Cys Asn	NO:2 Arg -5 Ser Trp His	Arg Ser Asn Gly 45	Cys Asp 30 Glu	Lys 15 Trp Cys	Arg Ile Pro Gln	His Val Phe Thr 65 Pro	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/804,625

DATE: 01/11/2002 TIME: 22:10:29

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		inful SEI: S
153		
154	Thr Glu	Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys
155		85 90 95
156	ובע ובע	Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys
157		
158 159		100 105 110
160	7 ~~	
161	Arg	
162		
163		
164	(2) INFO	RMATION FOR SEQ ID NO:3:
165	(2) INIO	MATION FOR BEQ ID NO.3.
166	(i)	SEQUENCE CHARACTERISTICS:
167	1-7	(A) LENGTH: 1607 base pairs
168		(B) TYPE: nucleic acid
169		(C) STRANDEDNESS: double
170		(D) TOPOLOGY: linear
171		(0) 10101000 -111001
172	(ii)	MOLECULE TYPE: cDNA to mRNA
173	·•	
174	(iii)	HYPOTHETICAL: NO
175	, ,	
176	(iv)	ANTI-SENSE: NO
177		
178	(vi)	ORIGINAL SOURCE:
179		(A) ORGANISM: Homo Sapiens
180		(G) CELL TYPE: Osteosarcoma Cell Line
181		(H) CELL LINE: U-2OS
182		
183	(vii)	IMMEDIATE SOURCE:
184		(A) LIBRARY: U2OS cDNA in Lambda GT10
185		(B) CLONE: Lambda U2OS-39
186		
187	(viii)	POSITION IN GENOME:
188		(C) UNITS: bp
189		
190	(ix)	FEATURE:
191		(A) NAME/KEY: CDS
192		(B) LOCATION: 3561546
193	(4)	
194	(1X)	FEATURE:
195		(A) NAME/KEY: mat_peptide (B) LOCATION: 12021543
196		(B) LOCATION: 12021543
197 198	(iz)	FEATURE:
198	(TX)	(A) NAME/KEY: mRNA
200		(B) LOCATION: 141607
200		(D) DOCATION. ITIOU/
202	(ix)	FEATURE:
203	(11)	(A) NAME/KEY: sig_peptide
204		(B) LOCATION: 356424
205		(-,

RAW SEQUENCE LISTING PATENT APPLICATION US/09/804,625

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206 207	(xi) SE	QUENCE DESCRI	PTION: SEQ	ID NO:3:		
208	,,					
209	стесьететь	CACTCTCTCT CAC	מראכידינים כידי	<u> </u>	GAACTTG CAGGGAGAAT	60
	GICGACICIA	GAGIGIGIGI CA	GCACIIGG CI	JGGGACII CIIC	SAACIIG CAGGGAGAAI	80
210	3 3 CERTOCOCO 3	GGGGA GMMMG GG	aaaamaaa mmi	T00000000 0000		700
211	AACTTGCGCA	CCCCACTTTG CG	CCGGTGCC TT	IGCCCCAG CGGA	AGCCTGC TTCGCCATCT	120
212						
213	CCGAGCCCCA	CCGCCCCTCC AC	TCCTCGGC CT	IGCCCGAC ACTO	GAGACGC TGTTCCCAGC	180
214						
215	GTGAAAAGAG	AGACTGCGCG GC	CGGCACCC GG	GAGAAGGA GGAG	GCAAAG AAAAGGAACG	240
216						
217	GACATTCGGT	CCTTGCGCCA GG	TCCTTTGA CC	AGAGTTTT TCC	ATGTGGA CGCTCTTTCA	300
218						
219	ATGGACGTGT	CCCCGCGTGC TTC	CTTAGACG GAG	CTGCGGTC TCCT	TAAAGGT CGACC ATG	358
220					Met	330
221					-282	
222		•			-262	
	ama aga aga		CDD CD3 CCC	mma ama amm	GGG GRG GRG	405
223					CCC CAG GTC CTC	406
224	-				Pro Gln Val Leu	
225	-280	•	-275	-270)	
226				•		
227	CTG GGC GGC	GCG GCT GGC	CTC GTT CCG	GAG CTG GGC	CGC AGG AAG TTC	454
228	Leu Gly Gly	, Ala Ala Gly 1	Leu Val Pro	Glu Leu Gly	Arg Arg Lys Phe	
229	-265	-260		-255	-250	
230						
231	GCG GCG GCG	TCG TCG GGC	CGC CCC TCA	TCC CAG CCC	TCT GAC GAG GTC	502
232			•		Ser Asp Glu Val	
233		-245	9	-240	-235	
234		245		240	. 233	
235	OTTO 300 030	. mma aza mma <i>i</i>	aca ama ama	3 CC 3 TC TTC	CCC CMC AAA CAC	550
					GGC CTG AAA CAG	550
236	Leu ser Gru		-		Gly Leu Lys Gln	
237		-230	-22)	-220	
238					• •	
239	AGA CCC ACC	CCC AGC AGG	GAC GCC GTG	GTG CCC CCC	TAC ATG CTA GAC	598
240	Arg Pro Thr	Pro Ser Arg	Asp Ala Val	Val Pro Pro	Tyr Met Leu Asp	
241	-21	.5	-210		-205	•
242						
243	CTG TAT CGC	AGG CAC TCA	GGT CAG CCG	GGC TCA CCC	GCC CCA GAC CAC	646
244	Leu Tvr Arg	Arq His Ser (Glv Gln Pro	Gly Ser Pro	Ala Pro Asp His	
245	-200	_	-195	-190	-	
246						
247	רכם דדם מאם	י אכם ככא ככם ז	אמת תמא מתת	אאר ארש פשפ	CGC AGC TTC CAC	691
247						694
_	-	=	ser arg ara		Arg Ser Phe His	
249	-185	-180		-175	-170	•
250						
251					GGG AAA ACA ACC	742
252	His Glu Glu		Glu Leu Pro	Glu Thr Ser	Gly Lys Thr Thr	
253		-165		-160	-155	
254						
255	CGG AGA TTC	TTC TTT AAT	TTA AGT TCT	ATC CCC ACG	GAG GAG TTT ATC	790
256					Glu Glu Phe Ile	_
257	5 5	-150	-145		-140	
258						